Evaluation of FAST-Prep™ PBC: an automated and rapid system for isolating microbial cells from positive blood culture

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INTRODUCTION

Sepsis is a serious condition associated with high mortality rate when not promptly treated. The current conventional diagnostic workflow requires species identification (ID) and antibiotic susceptibility test (AST) which may require up to 72 hours. Therefore, rapid diagnostic methods constitute a key approach to reduce identification and AST results. In this scenario, we aimed to evaluate FAST-PrepTM PBC, a rapid system for isolating microbial cells from positive blood culture resulting in a Liquid Colony™ (LC) which may be used for ID and AST.

METHODS

For the analysis 2 ml of PBC collected from Careggi University Hospital was transferred into the FAST-Prep™ cartridge and processed. LC and SOC isolate ID was carried out by MALDI-Tof MS (Biotyper, Bruker Daltonics, Bremen, Germany) and AST for GPB, GNB and anaerobic strain was performed with specific commercial Merlin panels (Merlin Diagnostika GmbH) (Figure 1) and interpreted according to EUCAST clinical breakpoints (v.11.0). ID was perfomed by adding 1 µl of formic acid to 1 µl of LC. In case of discrepant results between LC and SOC, ID and AST were repeated using LC culture seed. Moreover, when the discrepancy persist, AST was further repeated from SOC. Polymicrobial samples were not included in the study.

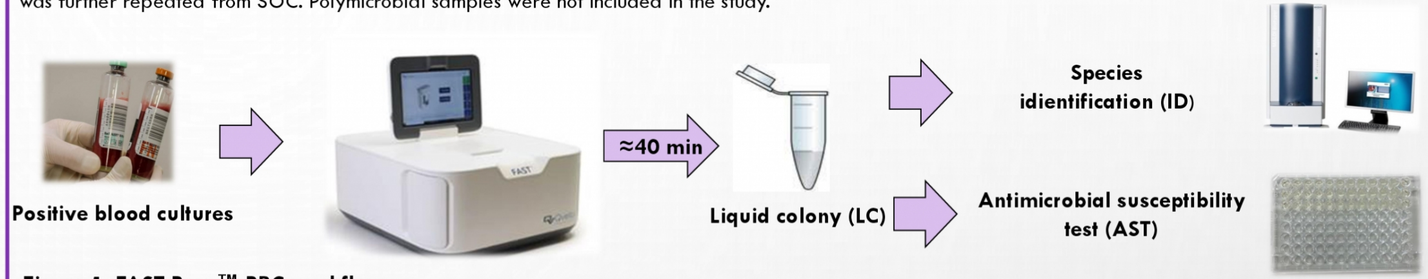
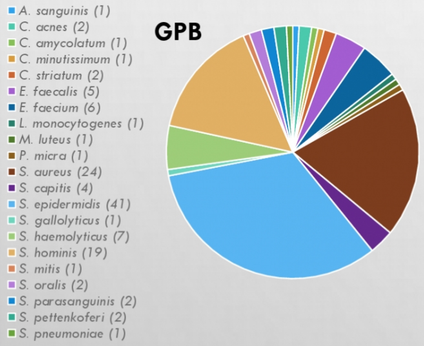


Figure 1: FAST-Prep™ PBC workflow

RESULTS

A total of 229 samples were included in the study. The collection was mainly composed of coagulase negative staphylococci (73) for Gram-positive isolates and of *Enterobacterales* species (82) for Gram-negative strains (Figure 2). Concordant ID between LC and SOC was detected in 204/229 (89%); 5/229 (3.5%) were discordant; and no ID was obtained in 20/229 (8.7%) samples (Figure 3).

Total drug-bug combinations tested were 5872 Gram-negative bacteria (GNB) and Gram-positive bacteria (GPB). Results for GNB showed a categorical agreement (CA) of 99.6% (2715/2724), with minor error (me), major error (ME), and very major error (VME) rates of 0.1% (3/2724), 0.1% (3/2007), and 0.4% (3/716), respectively. Results from GPB showed a CA of 99.6% (3138/3148) with me and ME rates of 0.2% (5/3148) and 0.2% (5/2341), respectively (Figure 4). CA according to the acceptability criteria of ISO 20776-2:2007.



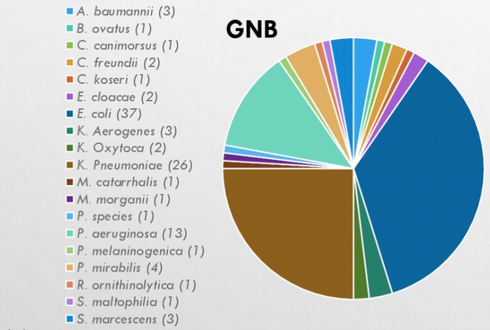


Figure 2: Species (Nr of isolates) included in the study.

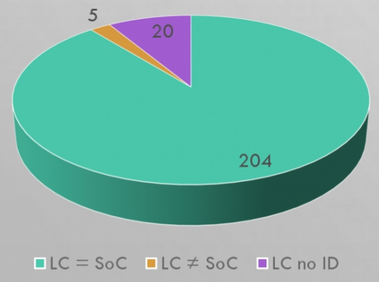


Figure 3: Comparison between ID using LC and SoC

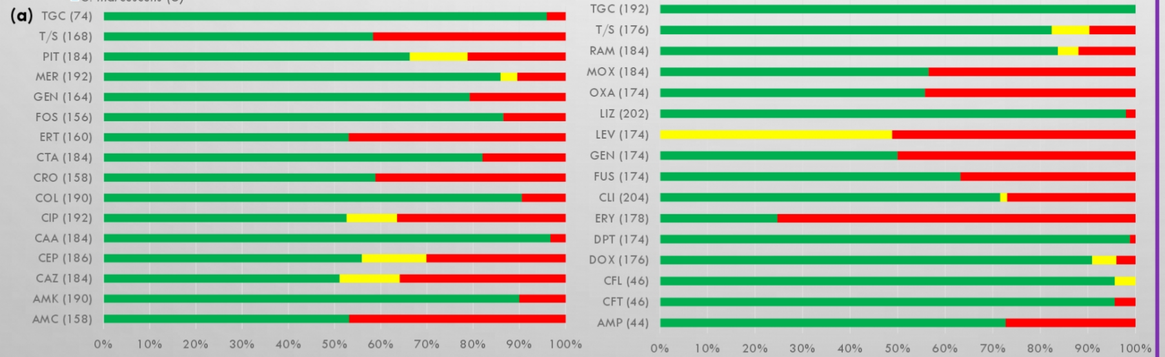


Figure 4: AST results on Gram-negative strains (a) and Gram-positive strains (b).

AMC: Amoxicillin/Clavulanic acid; AMK: Amikacin; AMP: Ampicillin; CAA: Ceftazime/Avibactam; CAZ: Ceftazidime; CEP: Cefepime; CFL: Ceftarolin; CFT: Ceftobiprole; CIP: Ciprofloxacin; CLI: Clindamycin; CRO: Ceftriaxone; CTA: Ceftolozane/Tazobactam; CTX: Cefotaxime; DPT: Daptomycin; DOX: Doxicycline; ERT: Ertapenem; ERY: Erythromycin; FOS: Fosfomycin; FUS: Fusidic Acid; GEN: Gentamicin; IMP: Imipenem; LEV: Levofloxacin; LIZ: Linezolid; MER: Meropenem; MOX: Moxifloxacin; MTR: Metronidazole; OXA: Oxaciclin; PIT: Piperacillin/Tazobatam; RAM: Rifampicin; TZD: Tedizolid; TPL: Teicoplanin; TGC: Tigecycline; T/S: Trimetophrim/Sulfametoxezole; VAN: Vancomycin.

CONCLUSIONS

These data demonstrate a high agreement between LC and SOC for both ID and AST. FAST-Prep™ allowed species identification in only 2 hours after blood culture's positivization and reduces AST response up to 24 hours in order to provide prompt targeted therapy (Figure 5). Moreover, interesting results were obtained also in case of anaerobic microorganisms whose ID may be more challenging since they require a loger incubation time of about 24 hours.

Further studies will be also interesting in order to evaluate additional application of the LC, such as immunochromatographic assays for the rapid detection of antimicrobial resistant determinants.

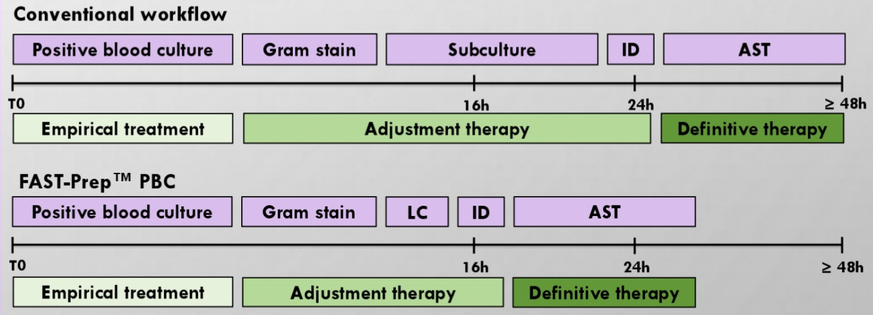


Figure 5: Comparison of conventional and FAST-Prep™ PBC workflows time-to-result

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